

LA-UR-14-26167

Approved for public release; distribution is unlimited.

Title: Understanding Host Pathogen Interactions: a Foundation for Advanced Therapeutics

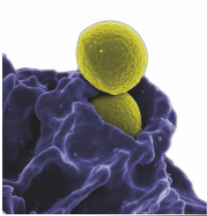
Author(s): Ribeiro, Ruy Miguel

Intended for: "Advanced Therapeutics" deep dive to be held at the Study Center at LANL on 08/05/2014

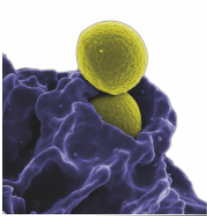
Issued: 2014-08-04

Disclaimer:

Los Alamos National Laboratory, an affirmative action/equal opportunity employer, is operated by the Los Alamos National Security, LLC for the National Nuclear Security Administration of the U.S. Department of Energy under contract DE-AC52-06NA25396. By approving this article, the publisher recognizes that the U.S. Government retains nonexclusive, royalty-free license to publish or reproduce the published form of this contribution, or to allow others to do so, for U.S. Government purposes. Los Alamos National Laboratory requests that the publisher identify this article as work performed under the auspices of the U.S. Department of Energy. Los Alamos National Laboratory strongly supports academic freedom and a researcher's right to publish; as an institution, however, the Laboratory does not endorse the viewpoint of a publication or guarantee its technical correctness.

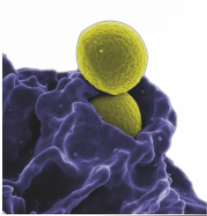


Understanding Host Pathogen Interactions: a Foundation for Advanced Therapeutics



Why “host-pathogen interactions”?

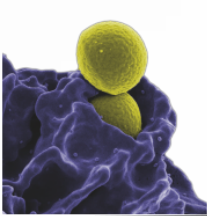
- We need new antibacterial / antiviral compounds
 - New threats
 - Resistance
- In the post-genomics era we can rationally target key host-pathogen pathways
- Potential for broad spectrum
 - Phylogenetically related, emergent threats



Why LANL?



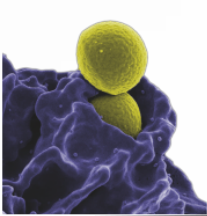
- Scientific and technological foundation
- Capability for multidisciplinary approach
 - From screening to modeling
- Capability for a sustained effort
- Basic science problem
 - Initially, too hard for “private companies”



LANL Science / Technology Foundation

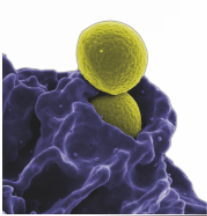


- Technology: development and use
 - Automation
 - High throughput
 - State-of-the-art assays
- Science
 - Bacterial pathogenicity
 - Innate immunity
 - Identifying new host-pathogen interactions
 - Modeling: from statistics to bioinformatics to mechanistic models



A few examples

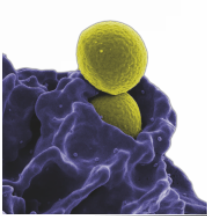




A few examples

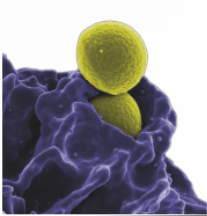


- Influenza
- Burkholderia

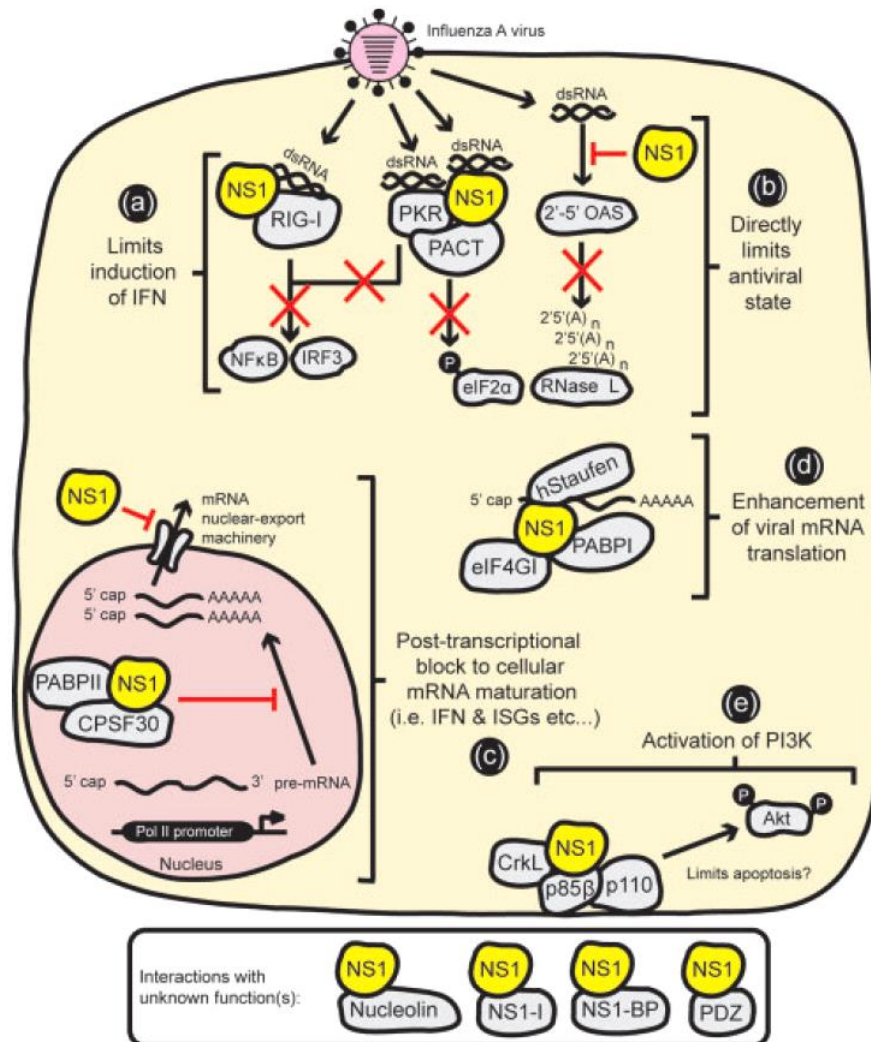


Protein-Protein Interactions

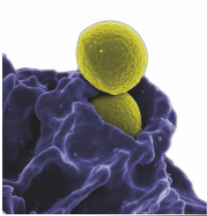
- Are involved in multiple pathogenic pathways
 - Cleavage of pathogen proteins (e.g., influenza)
 - Toxin effects (e.g., *B. anthracis*)
 - Disruption of innate immunity (e.g., influenza, HCV, ...)
 - Promote cell entry (e.g., *Burkholderia spp*)



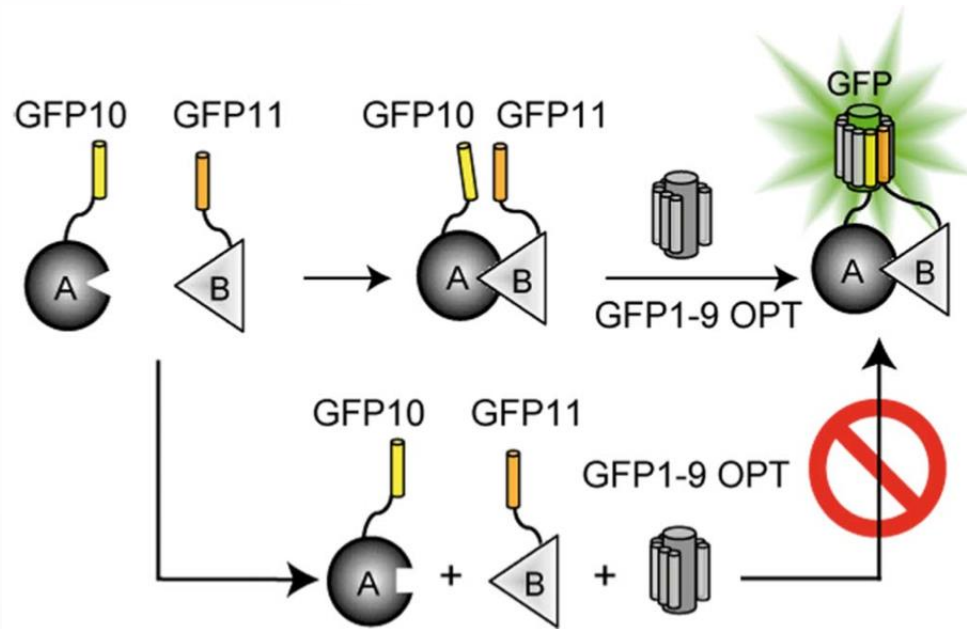
Influenza A NS1 effector/host biology



- NS1 disrupts innate immune responses
- NS1 interacts with multiple host proteins
 - Binds p85 β /p110 complex and limits apoptosis

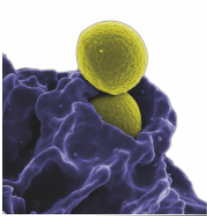


Tracking interactions: *tripartite* GFP



- Attach small 15aa tags to proteins (GFP strands 10 and 11)
- Interaction status is polled by expressing GFP 1-9
- Extensively engineered to not perturb passenger proteins

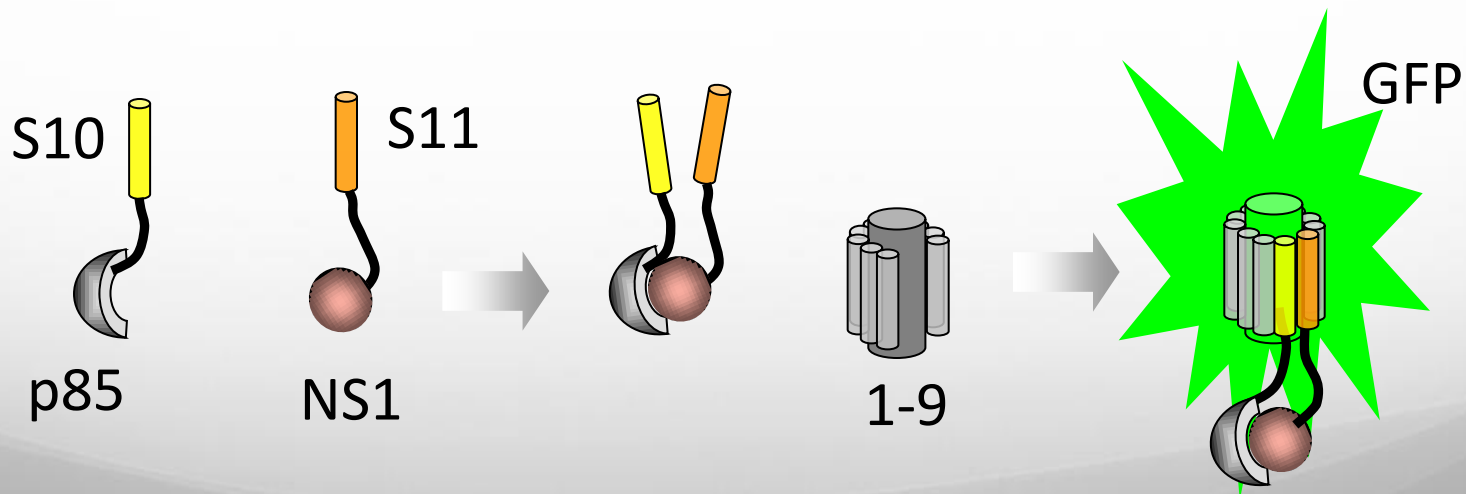
Cabantous S. et. al, 2013 Sci Rep 3,
doi:10.1038/srep02854

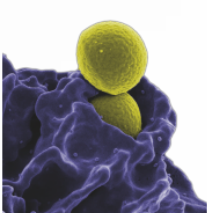


Proof of principle



- NS1 interacts with p85 β but not p85 α
- A single point mutation (M582V) converts p85 α into an NS1 interactor: gain-of-function mutation
- A single point mutation (Y89F) converts NS1 into a non-interactor
- Can we detect these small sequence changes?





GFP based assay



Cell lysates

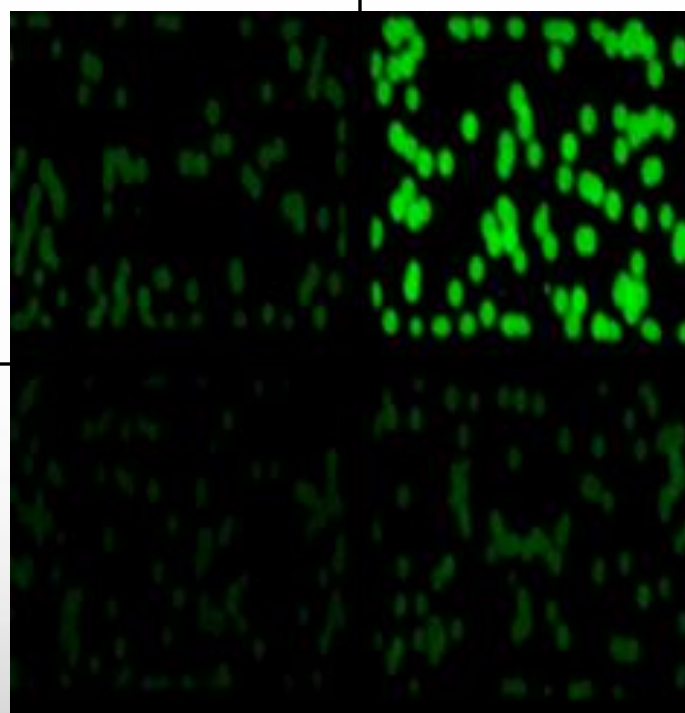
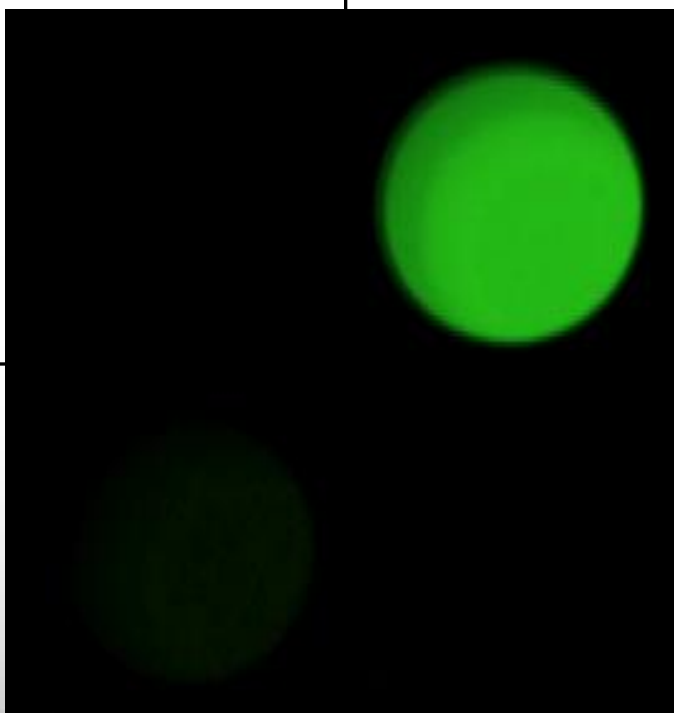
E. coli colonies

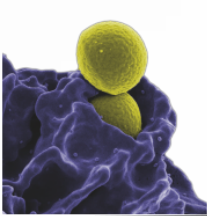
NS1 Y89F NS1

NS1 Y89F NS1

p85α
M582V

p85α

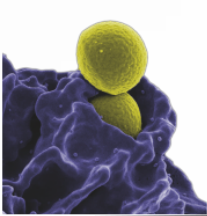




Advantages of tripartite split GFP



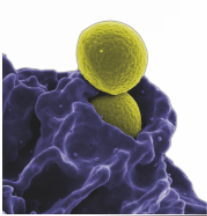
- Small tags: minimize disruption of protein function
- High sensitivity
- Applicable *in vivo*
- Soluble, not temperature dependent
- Spatial resolution



Disrupting host pathogen interactions



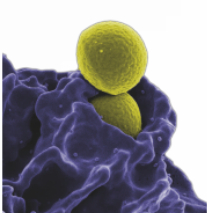
**Direct visualization of crucial interactions for
pathogen survival / virulence**



Disrupting host pathogen interactions

Direct visualization of crucial interactions for pathogen survival / virulence

- Use RNA interference to knock down mRNA expression of target genes
- Target all genes (whole genome) or given pathway
- Measure effect of host mRNA knock down on viability / replication of pathogen



RNAi-based screen of *B. thailandensis* invasion

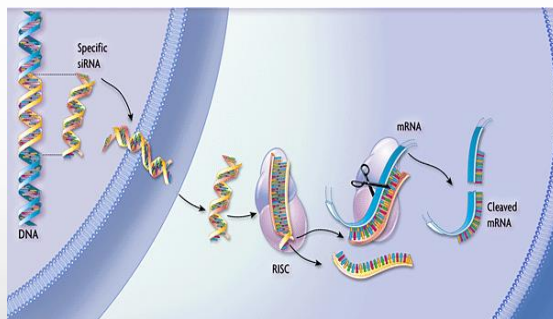


siRNA library for kinases

Targeting 782 kinases with
>2500 siRNA constructs



Gene knock-down in the host



Assay strategy

Host cell invasion by
GFP-labeled *B. thailandensis*

1) siRNAs
(72 hrs)



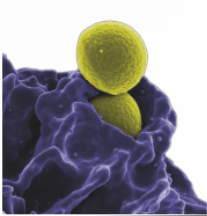
2) *B. thailandensis*
(MOI 10) (20 hrs)

THP-1



+ chloramphenicol

Read fluorescence in 96 well plates
using LSRII flow cytometer

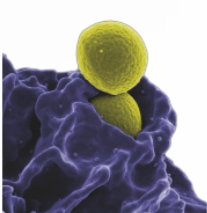


RNAi screen hits



Actin polymerization	Centrosome/spindle function Mitosis	Ca2+/Calmodulin	PKC / cAMP	PIP	Glycogenesis	RTK	Adhesion	NF-kB signaling
PAK3 STK35 PKN3 AKT2 STK11	AURKC, AURKA MAST3 UHMK1 STK22D, STK4 STK38L/NDR1	CAMK2B CAMK2A CAMK1G CALM1 CAMKK2	PKCη PRKACB	P101-PI3K ITPKA PIK3R1 PIP5K1A PIP5K2B AKT1	INSRR PCK1 HK1 HK2 HK3	KDR EPHA3 EPHB3 TYRO3 ERBB3	PTK7 ABL1	MAP2K7 MAP3K2 MAP3K11 MAPK6

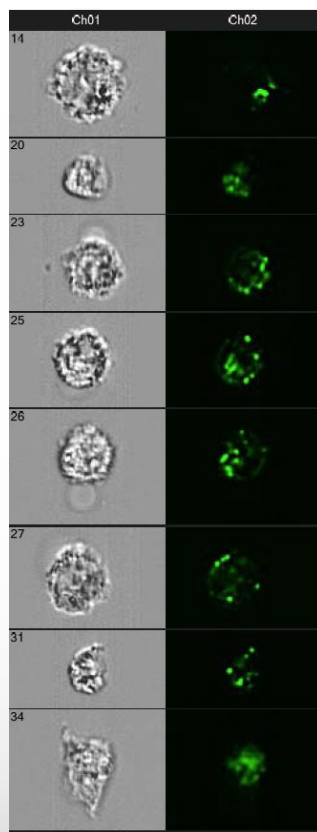
- Identified ~40 host genes required for entry and intracellular growth of *B. thailandensis*
- Candidate genes classified into multiple interconnected host pathways – some common to infections with other pathogens (e.g. ABL1, AKT1)
- Validate candidate hits using imaging flow cytometry and microscopy



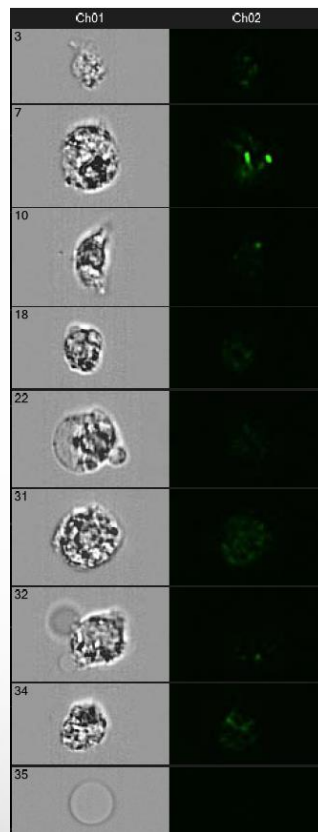
Validation using Imaging flow cytometry



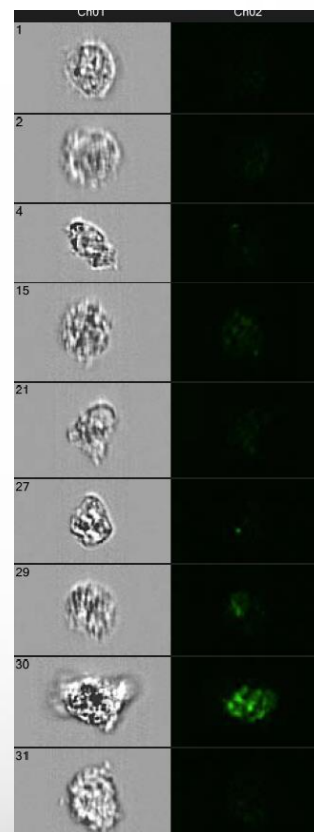
THP-siRNA-Control

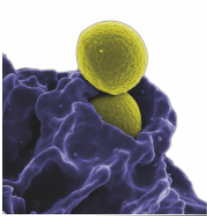


THP-siRNA-MAP3K11

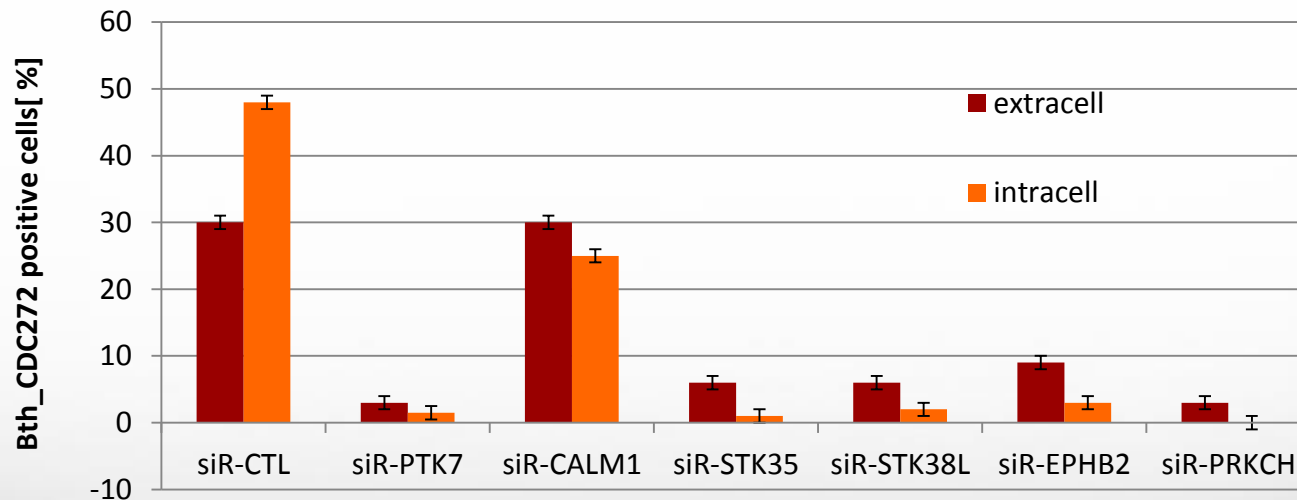
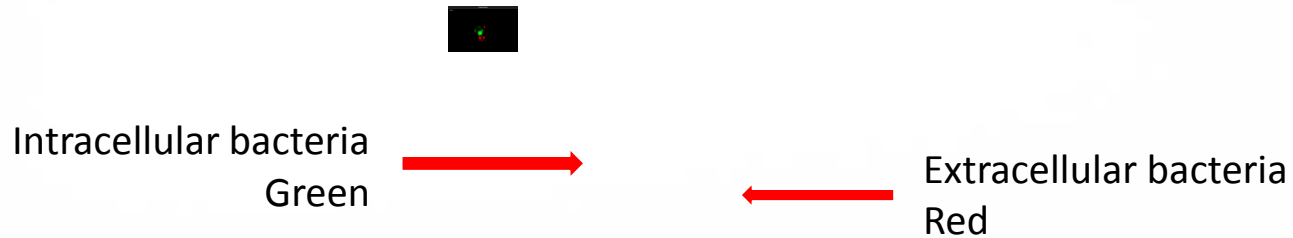


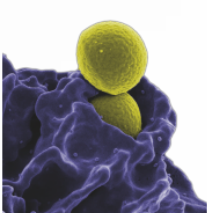
THP-siRNA PIP5K1A





Labeling extra vs intracellular *B. thailandensis*





PKC η probably acts through MARCKS

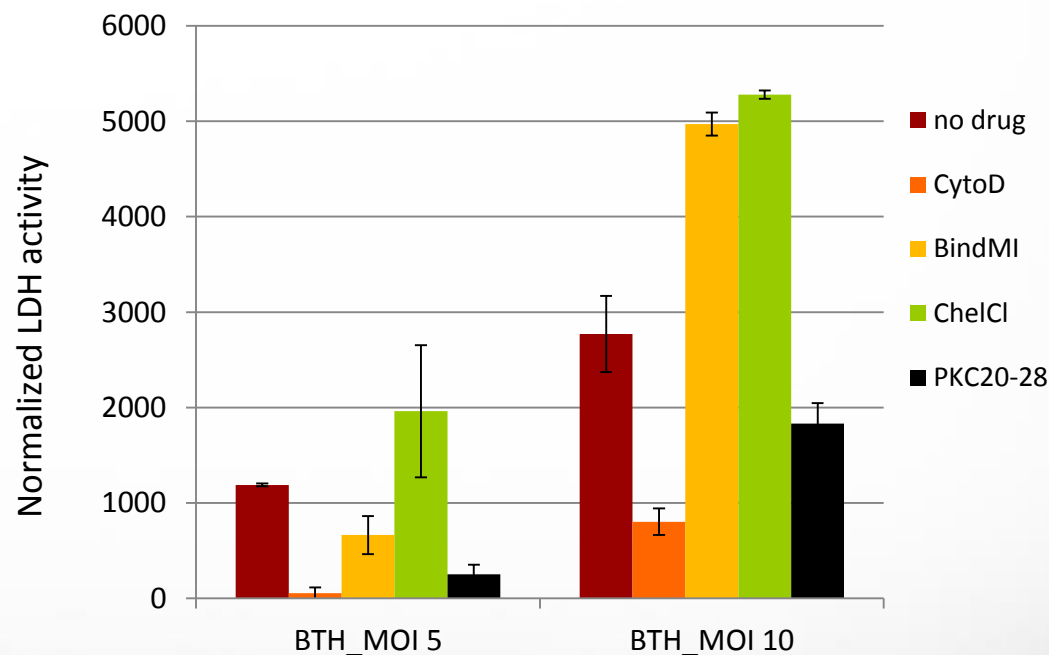


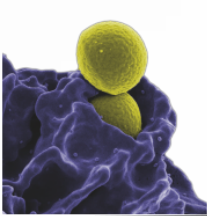
PKC η – Protein kinase C-eta

- Regulated by diacylglycerol and phosphatidylserine, but not calcium
- Previously implicated in *Listeria* and *Plasmodium* infection

MARCKS - myristoylated alanine-rich protein kinase C substrate

- An actin filament crosslinking protein
- Cell motility, phagocytosis, membrane trafficking and mitogenesis

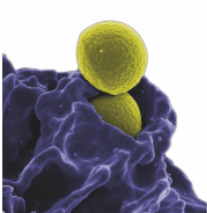




Conclusions



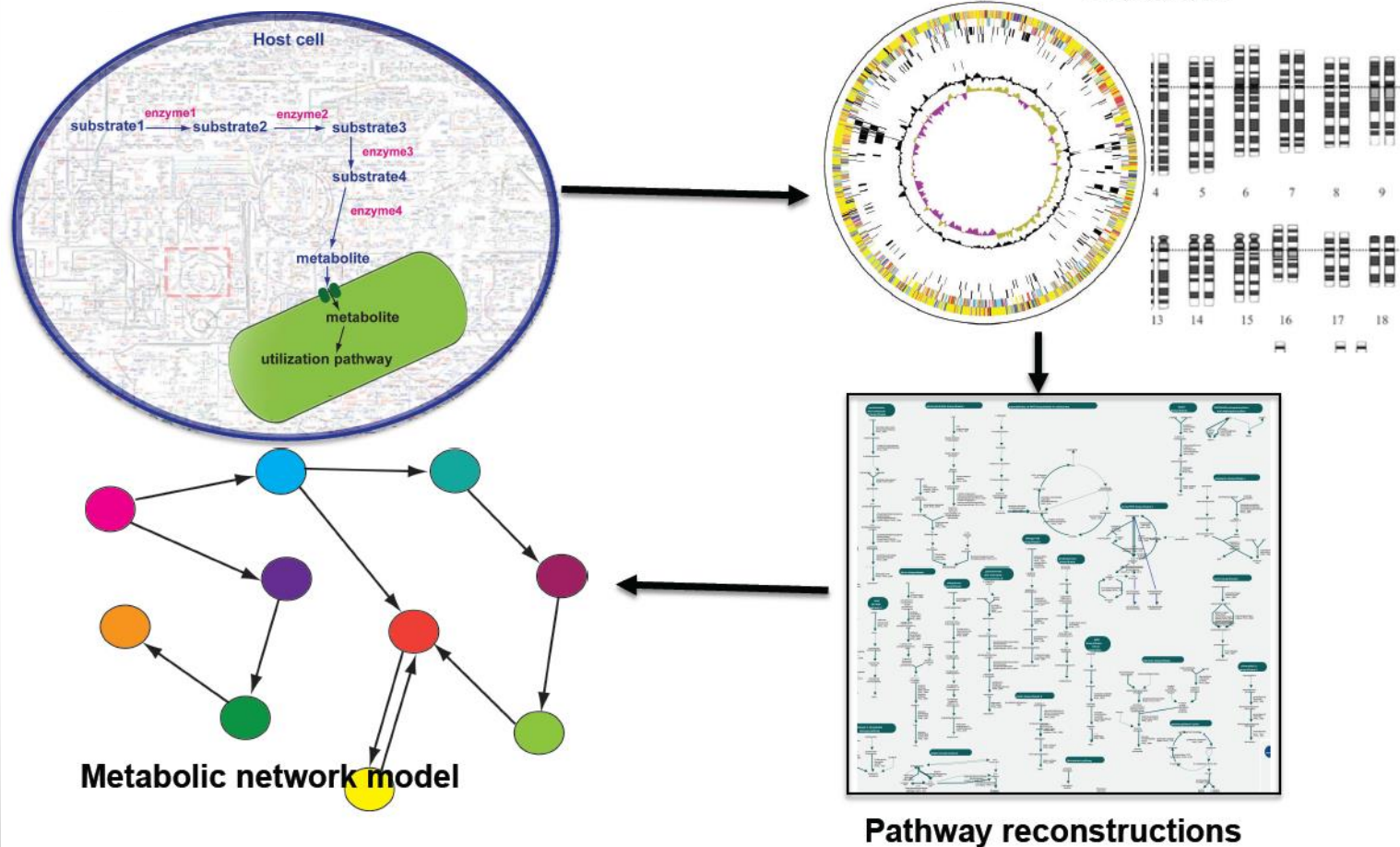
- We have identified ~40 kinases that regulate *Burkholderia* invasion in the host.
- Small molecules that are FDA approved for cancer treatment can be repurposed / tested as antimicrobials
- We have applied the same ideas to an extracellular pathogen
 - *Yersinia spp*: BMC Microbiology 2013, 13:249

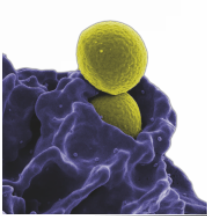


Host-pathogen metabolic interactions



Burkholderia pseudomallei

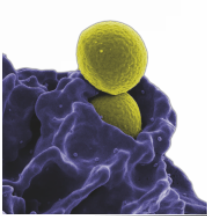




Host response as a pathogen detector



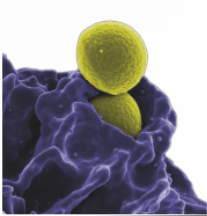
Different influenza strains will produce individual response profiles



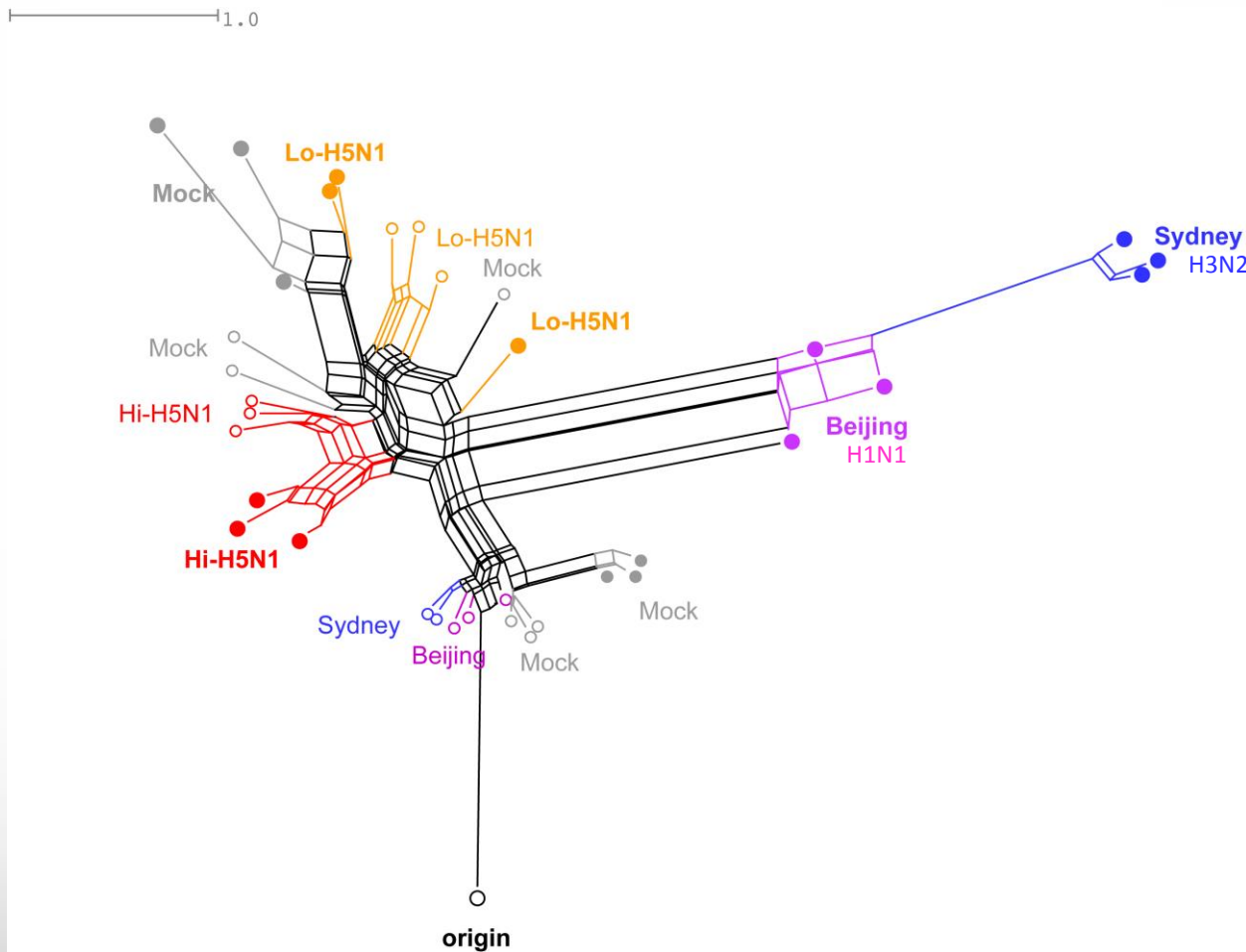
Host response as a pathogen detector

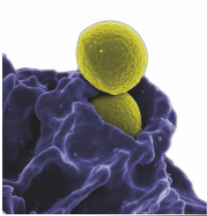
Different influenza strains will produce individual response profiles

- Primary human upper airway epithelial cells
- H5N1: A/HK/483/97 high pathogenic (HP) and A/HK/486/97 low pathogenic (LP) H5N1
- H1N1: A/Beijing/26/95; H3N2: A/Sydney/5/97
- Whole genome microarray
- 36 experiments: 4 strains, 3 time points, 3 repeats for each. 44,000 data points each experiment.

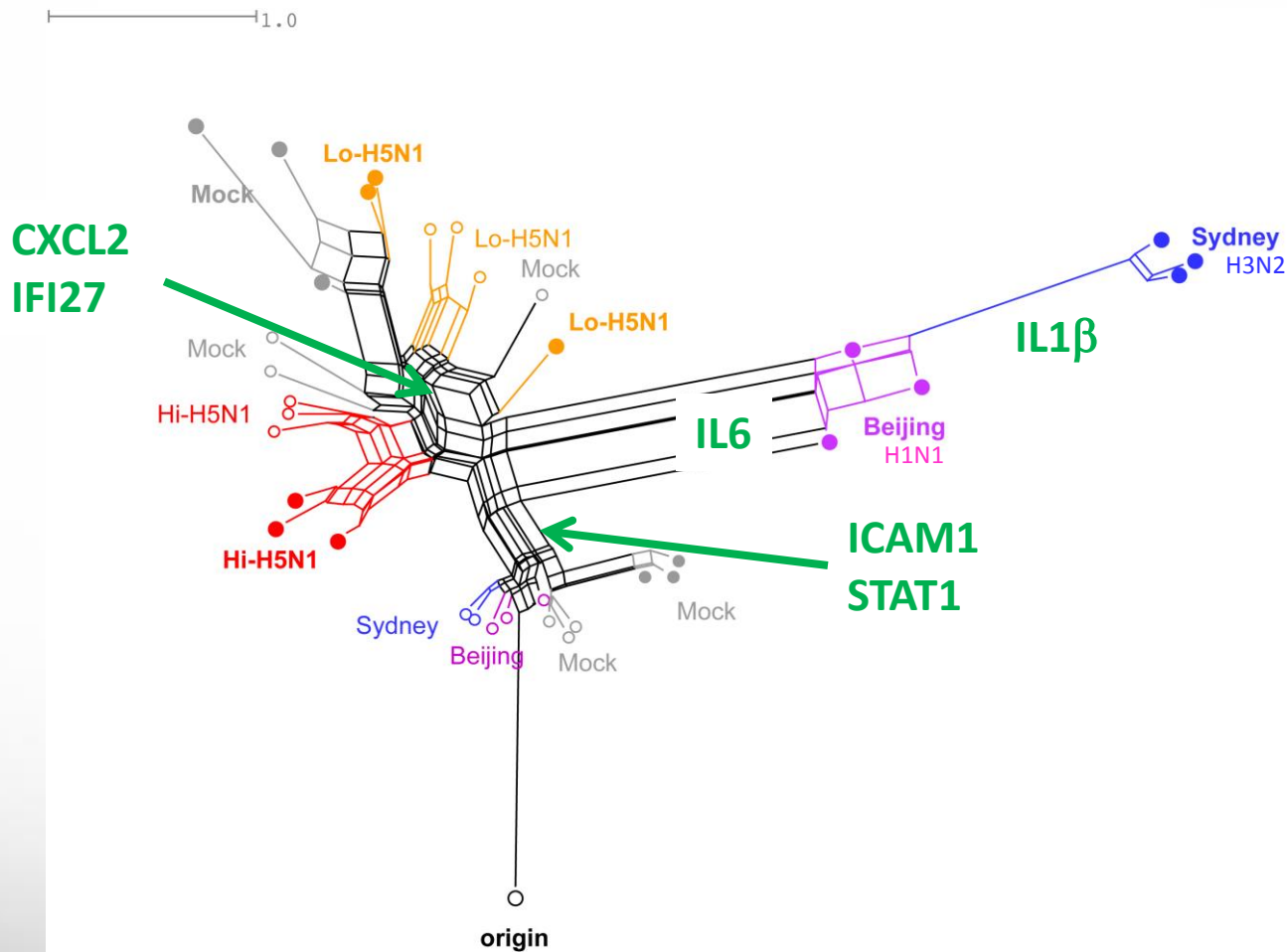


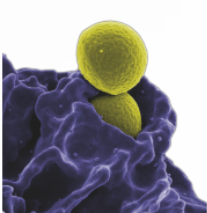
Host response as a pathogen detector



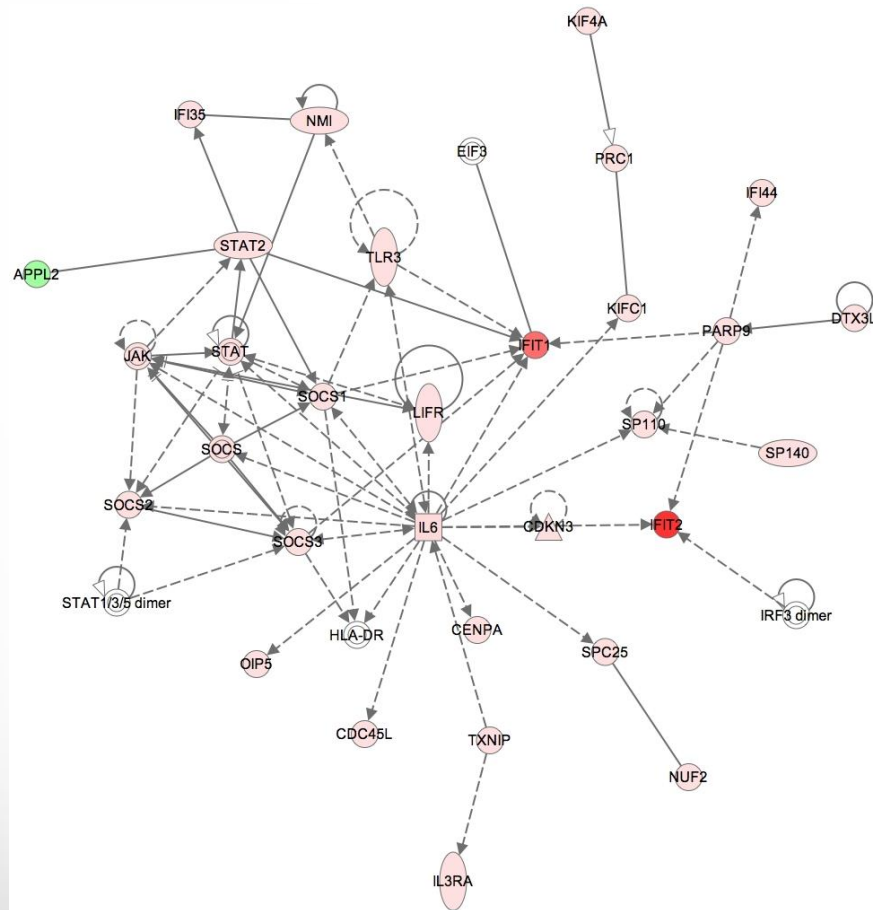


Host response as a pathogen detector

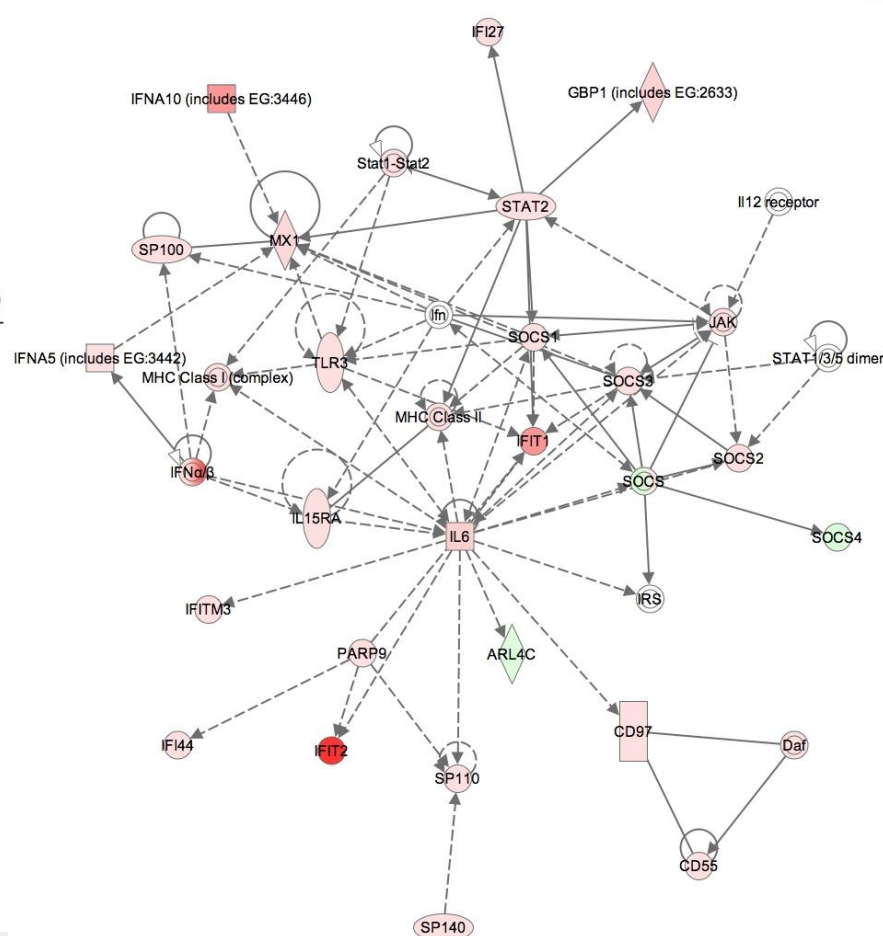




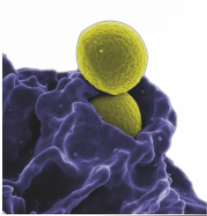
IL-6 mediated signaling network (24h)



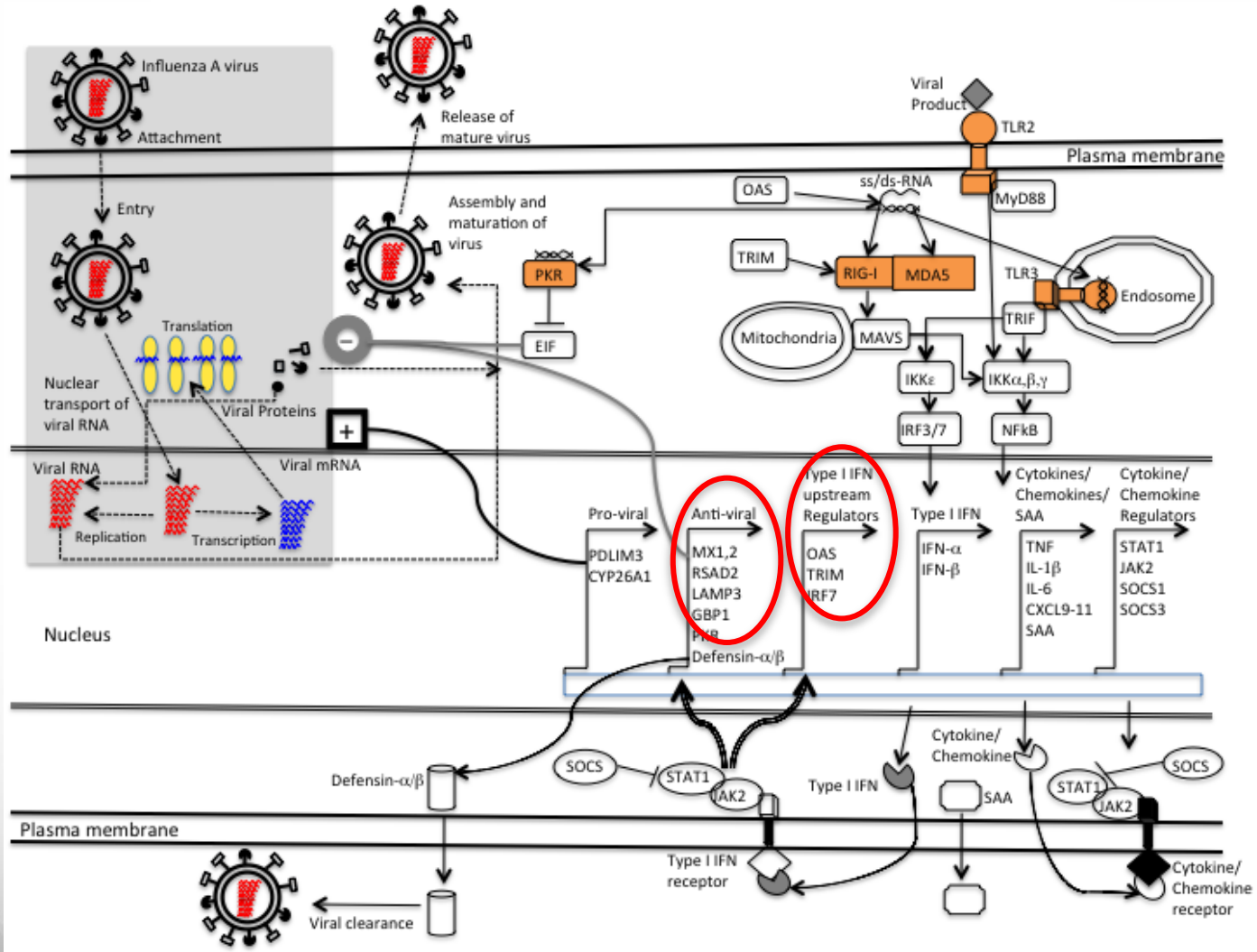
H1N1 (Beijing): Cell to cell signaling, cellular interactions, and endocytosis



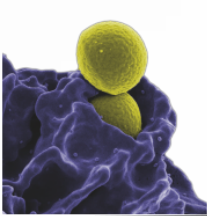
H3N2 (Sydney): Antigen presentation, antimicrobial response, and cell-mediated immune responses.



Validation (e.g., viral sensors pathways)



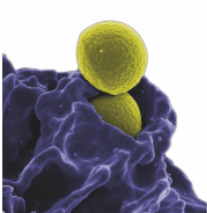
More
expressed
in H3N2
than in
H1N1



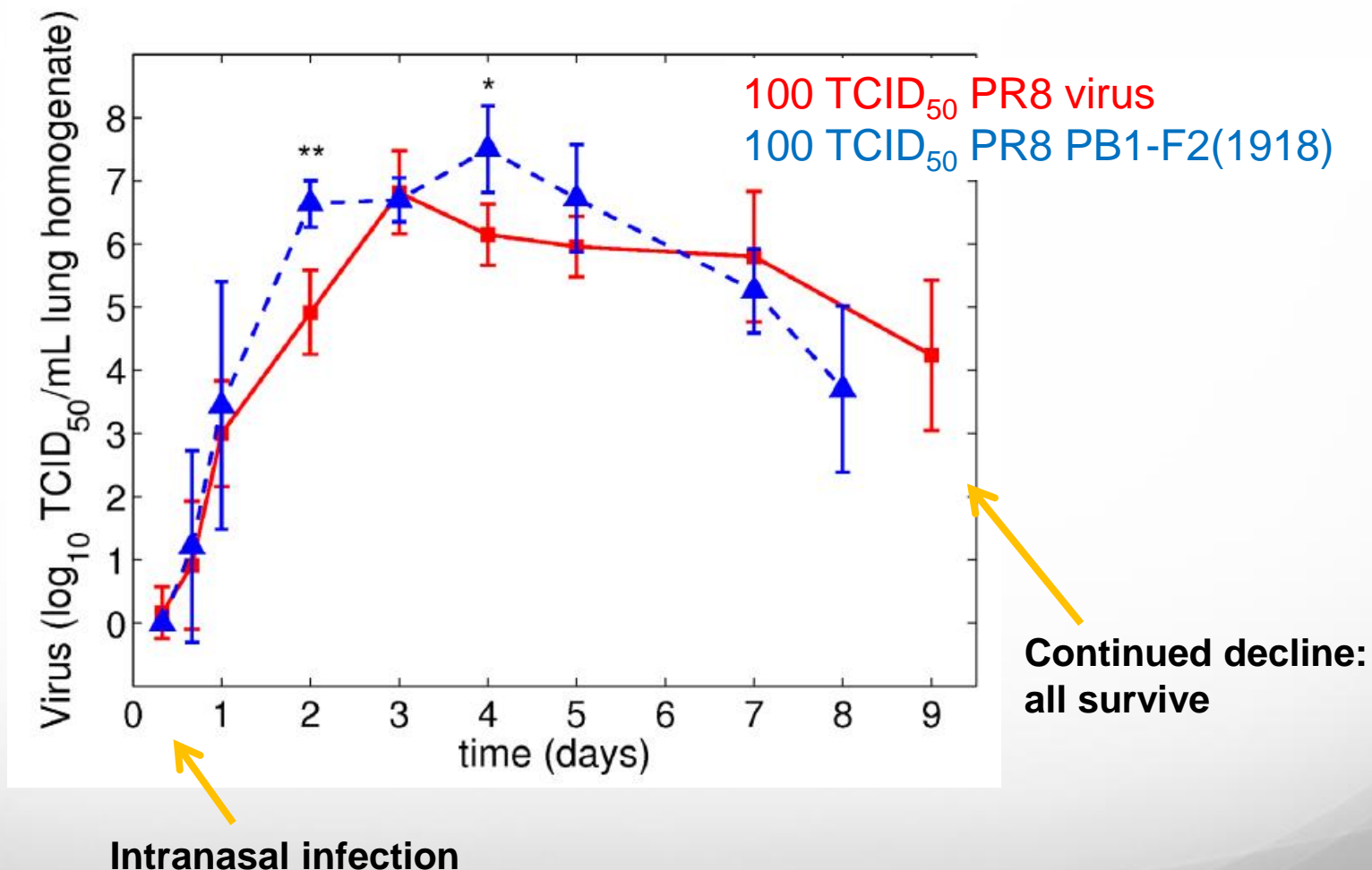
Modeling infection at the host scale

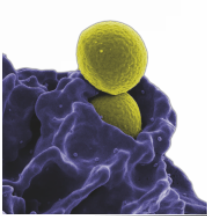


Host pathogen interactions can also occur at other scales: co-infection



Mouse model of influenza infection





Fits to influenza infection in mice

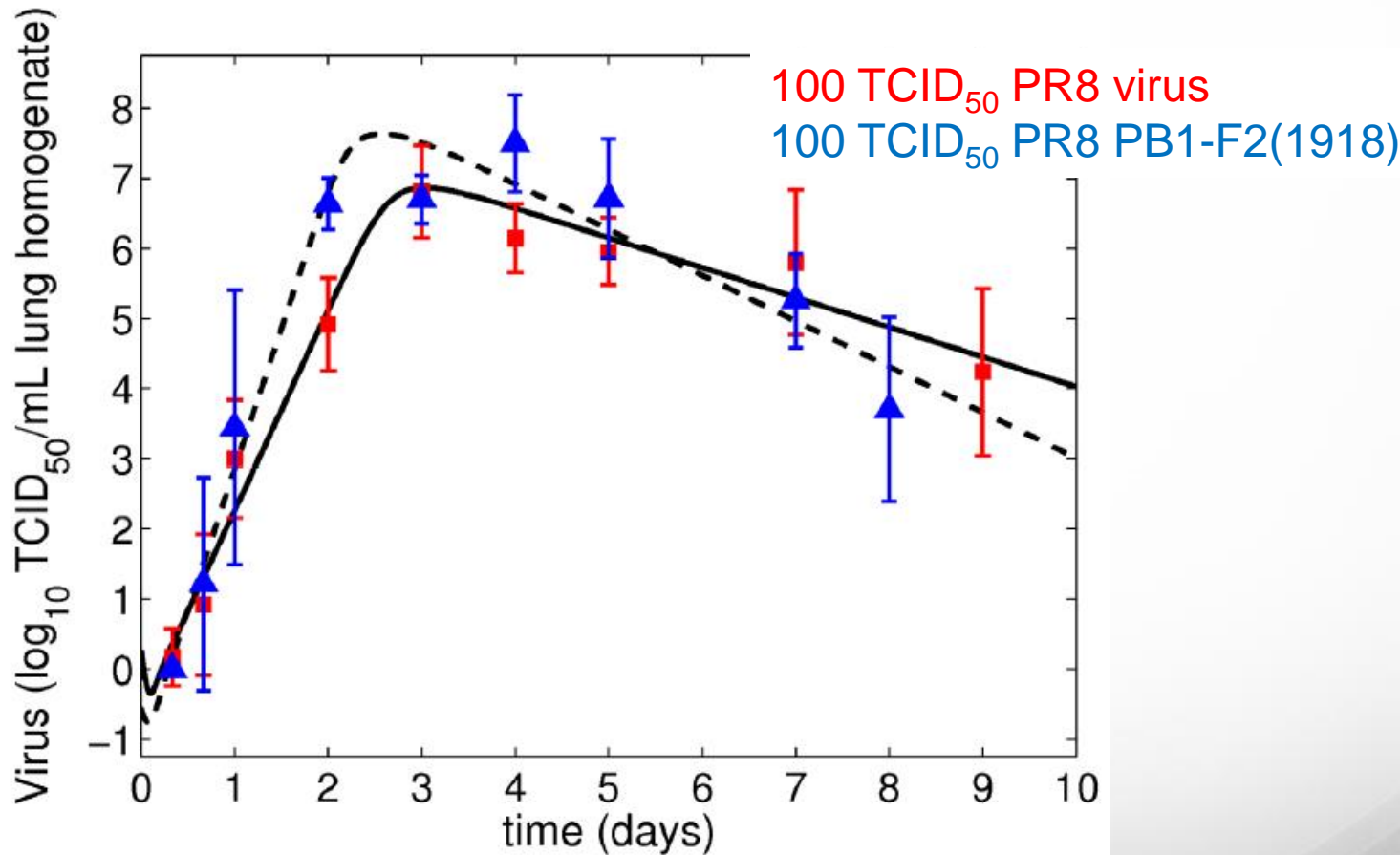


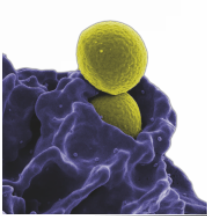
$$\frac{dT}{dt} = -\beta TV$$

$$\frac{dI_1}{dt} = \beta TV - kI_1$$

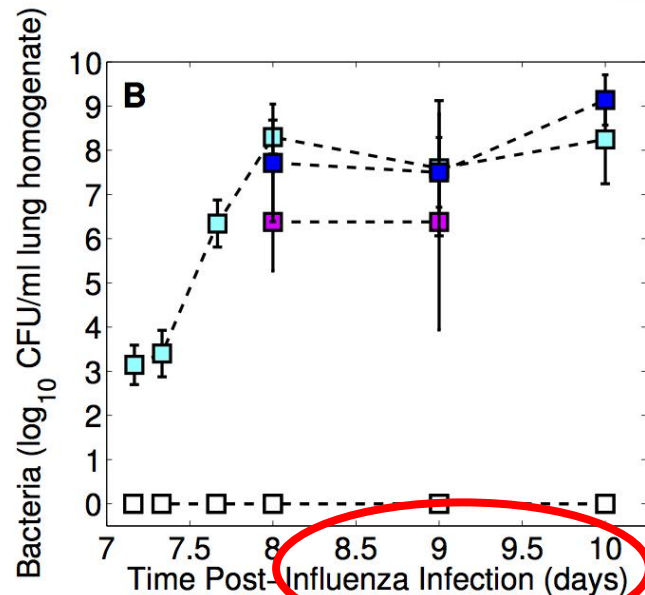
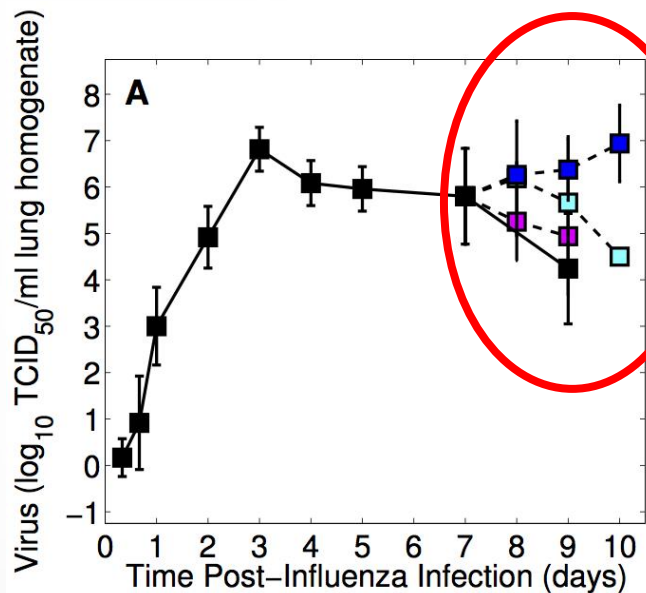
$$\frac{dI_2}{dt} = kI_1 - \delta I_2$$

$$\frac{dV}{dt} = pI_2 - cV$$





Effect of bacterial co-infection on titers



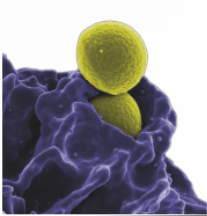
- PR8 + 100 CFU D39
- PR8 + 1000 CFU D39
- PR8 + 1000 CFU A66.1
- PR8 - No Bacteria
- D39 or A66.1 - No Virus



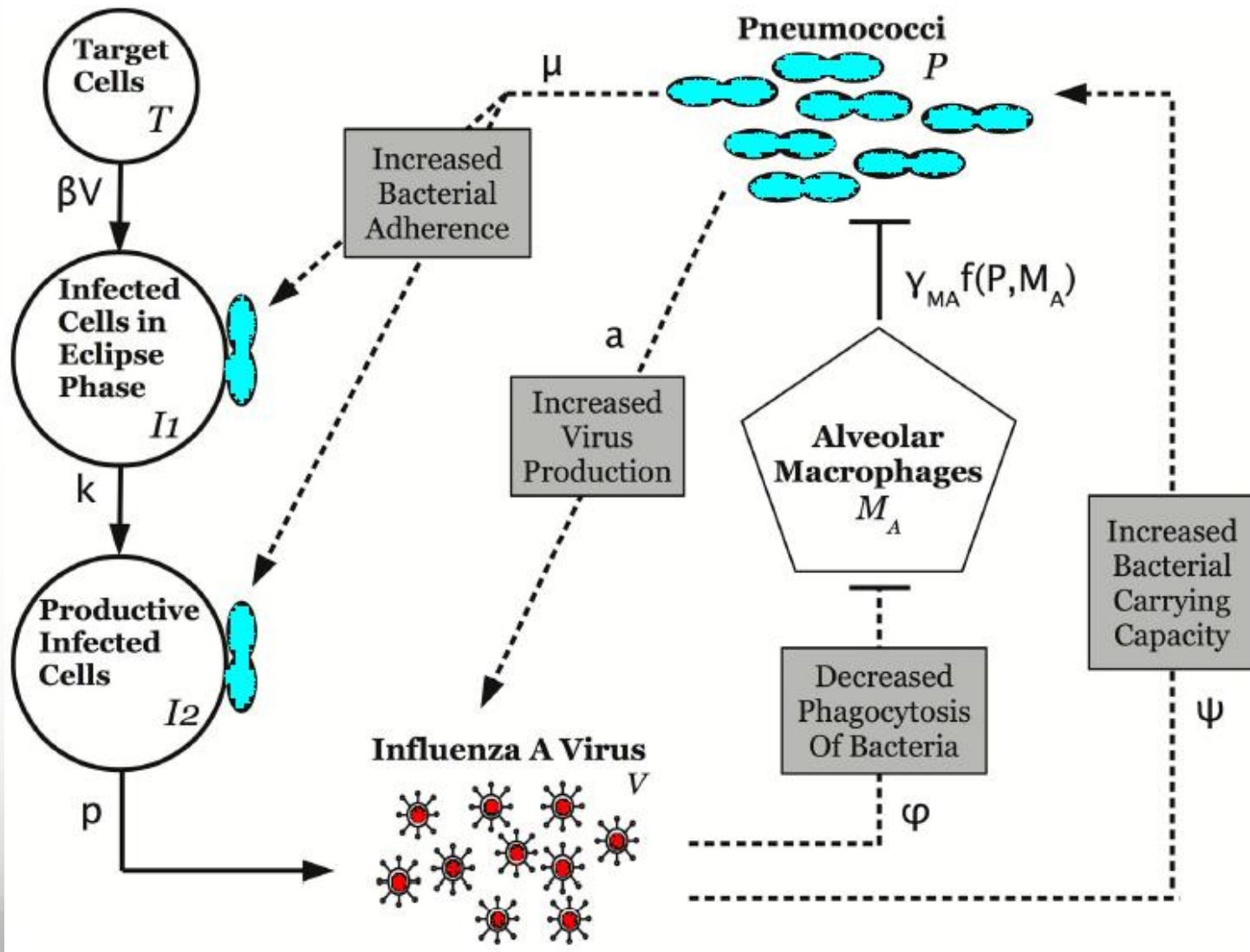
Bacterial challenge

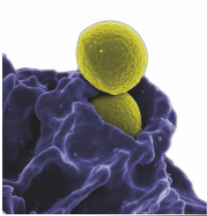


All mice euthanized

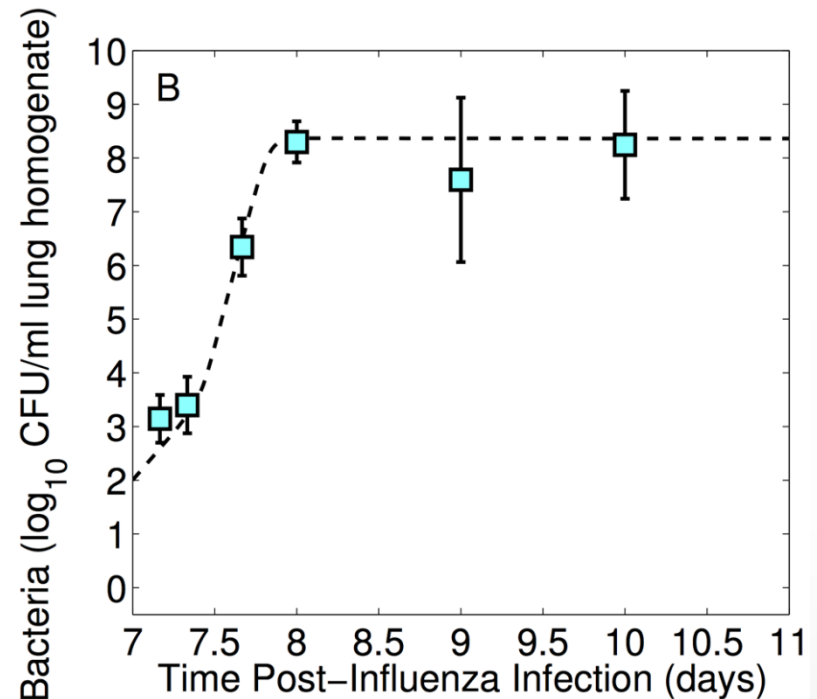
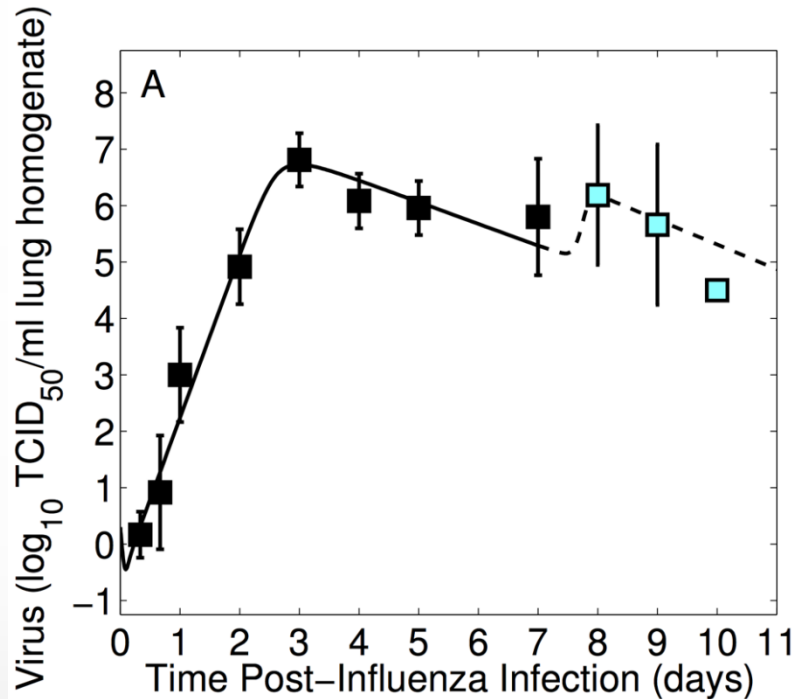


Modeling possible mechanisms

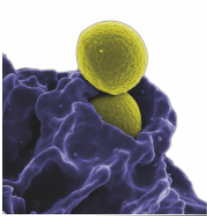




Model fits: PR8 and *S. pneumoniae*



Smith *et al.*, PLoS Path. 9: e1003238 (2013)

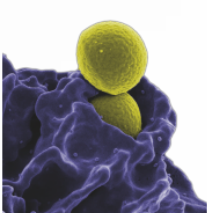


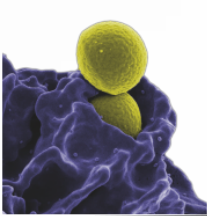
Results



Effect	Consequences	Hypothesis
Alveolar Macrophage Dysfunction	Decreased phagocytic ability, heterogeneity in individual lung titers, and loss of phagocytic cells and early innate immune signaling	Influenza-induces phenotypic changes and/or apoptosis in alveolar macrophages
Enhanced Viral Release from Infected Cells	Rebound of viral titers and altered immune responses	Bacterial proteases and/or neuraminidases affect viral release from infected cells

Recently shown to be a factor:
Ghoneim et al. J. Immunol 2013

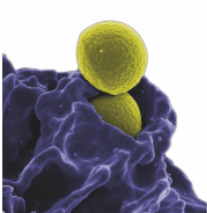




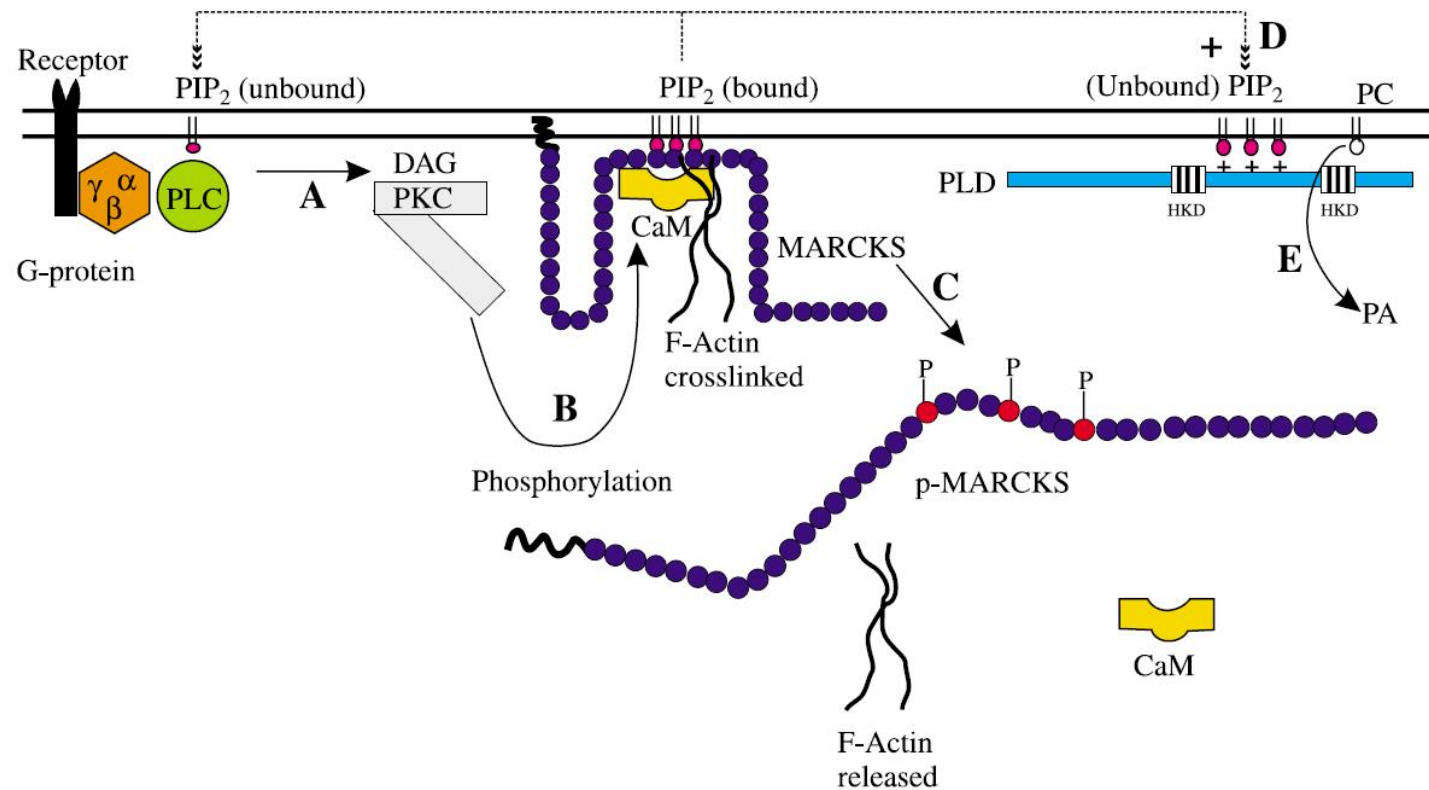
Future plans

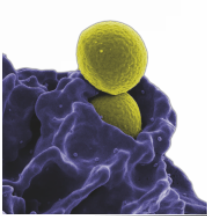


- **Approach**
 - Focus on key pathogens and key pathways
 - Multidisciplinary teams / external collaborators
 - Develop predictive models to integrate multiple data streams
- **Topics**
 - Determine how a pathogen subverts or coopts host immune pathways to propagate its lifecycle
 - Understand the immune modulatory effects of a pathogen
 - Capture host responses at the pre-symptomatic stage



Example I - *Burkholderia*

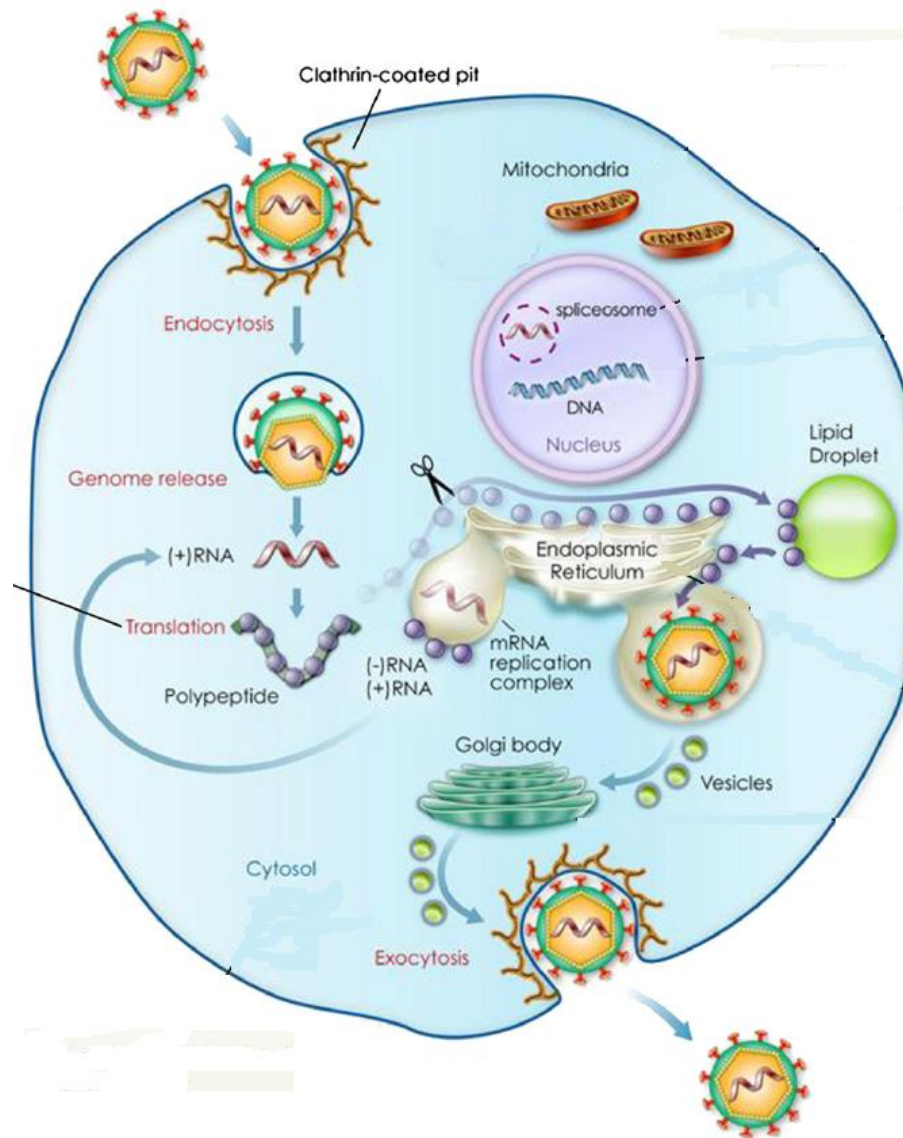


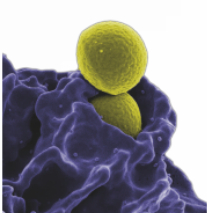


Example II – hepatitis C virus



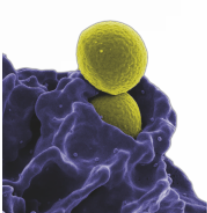
Cyclophilin A:
regulator of
translation

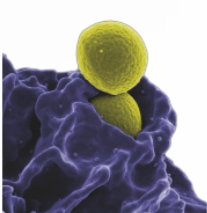


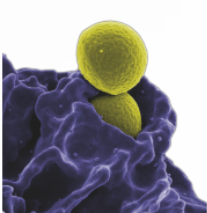


Impact









Targeting *Burkholderia* cellular invasion

